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NEWS	2	JUN 06	EPFULL enhanced with 260,000 English abstracts
NEWS	3	JUN 06	KOREAPAT updated with 41,000 documents
NEWS	4	JUN 13	USPATFULL and USPAT2 updated with 11-character patent numbers for U.S. applications
NEWS	5	JUN 19	CAS REGISTRY includes selected substances from web-based collections
NEWS	6	JUN 25	CA/CAPLUS and USPAT databases updated with IPC reclassification data
NEWS	7	JUN 30	AEROSPACE enhanced with more than 1 million U.S. patent records
NEWS	8	JUN 30	EMBASE, EMBAL, and LEMBASE updated with additional options to display authors and affiliated organizations
NEWS	9	JUN 30	STN on the Web enhanced with new STN AnaVist Assistant and BLAST plug-in
NEWS	10	JUN 30	STN AnaVist enhanced with database content from EPFULL
NEWS	11	JUL 28	CA/CAPLUS patent coverage enhanced
NEWS	12	JUL 28	EPFULL enhanced with additional legal status information from the epoLine Register
NEWS	13	JUL 28	IFICDB, IFIPAT, and IFIUDB reloaded with enhancements
NEWS	14	JUL 28	STN Viewer performance improved
NEWS	15	AUG 01	INPADOCDB and INPAFAMDB coverage enhanced
NEWS	16	AUG 13	CA/CAPLUS enhanced with printed Chemical Abstracts page images from 1967-1998
NEWS	17	AUG 15	CAOLD to be discontinued on December 31, 2008
NEWS	18	AUG 15	CAPLUS currency for Korean patents enhanced
NEWS	19	AUG 27	CAS definition of basic patents expanded to ensure comprehensive access to substance and sequence information
NEWS	20	SEP 18	Support for STN Express, Versions 6.01 and earlier, to be discontinued
NEWS	21	SEP 25	CA/CAPLUS current-awareness alert options enhanced to accommodate supplemental CAS indexing of exemplified prophetic substances
NEWS	22	SEP 26	WPIDS, WPINDEX, and WPIX coverage of Chinese and Korean patents enhanced
NEWS	23	SEP 29	IFICLS enhanced with new super search field
NEWS	24	SEP 29	EMBASE and EMBAL enhanced with new search and display fields
NEWS	25	SEP 30	CAS patent coverage enhanced to include exemplified prophetic substances identified in new Japanese-language patents
NEWS	26	OCT 07	EPFULL enhanced with full implementation of EPC2000
NEWS	27	OCT 07	Multiple databases enhanced for more flexible patent

number searching

NEWS EXPRESS JUNE 27 08 CURRENT WINDOWS VERSION IS V8.3,
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L3 ANSWER 1 OF 1 MEDLINE on STN DUPLICATE 1
 AN 1997084811 MEDLINE
 DN PubMed ID: 8931145
 TI Characterization of the S1 binding site of the glutamic
 acid-specific protease from *Streptomyces*
griseus.
 AU Stennicke H R; Birktoft J J; Breddam K
 CS Carlsberg Laboratory, Department of Chemistry, Copenhagen, Denmark.
 SO Protein science : a publication of the Protein Society, (1996 Nov) Vol. 5,
 No. 11, pp. 2266-75.
 Journal code: 9211750. ISSN: 0961-8368.
 CY United States
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals
 EM 199702
 ED Entered STN: 5 Mar 1997
 Last Updated on STN: 3 Mar 2000
 Entered Medline: 19 Feb 1997
 AB The glutamic acid-specific protease
 from *Streptomyces griseus* (SGPE) is an 18.4-kDa serine protease with a
 distinct preference for Glu in the P1 position. Other enzymes
 characterized by a strong preference for negatively charged residues in
 the P1 position, e.g., interleukin-1 beta converting enzyme (ICE), use Arg
 or Lys residues as counterions within the S1 binding site. However, in
 SGPE, this function is contributed by a His residue (His 213) and two Ser
 residues (Ser 192 and S216). It is demonstrated that proSGPE is activated
 autocatalytically and dependent on the presence of a Glu residue in the -1
 position. Based on this observation, the importance of the individual S1
 residues is evaluated considering that enzymes unable to recognize a Glu
 in the P1 position will not be activated. Among the residues constituting
 the S1 binding site, it is demonstrated that His 213 and Ser 192 are
 essential for recognition of Glu in the P1 position, whereas Ser 216 is
 less important for catalysis out has an influence on stabilization of the
 ground state. From the three-dimensional structure, it appears that His
 213 is linked to two other His residues (His 199 and His 228), forming a
 His triad extending from the S1 binding site to the back of the enzyme.
 This hypothesis has been tested by substitution of His
 199 and His 228 with other amino acid residues. The catalytic
 parameters obtained with the mutant enzymes, as well as the pH dependence,
 do not support this theory; rather, it appears that His 199 is responsible
 for orienting His 213 and that His 228 has no function associated with the
 recognition of Glu in P1.